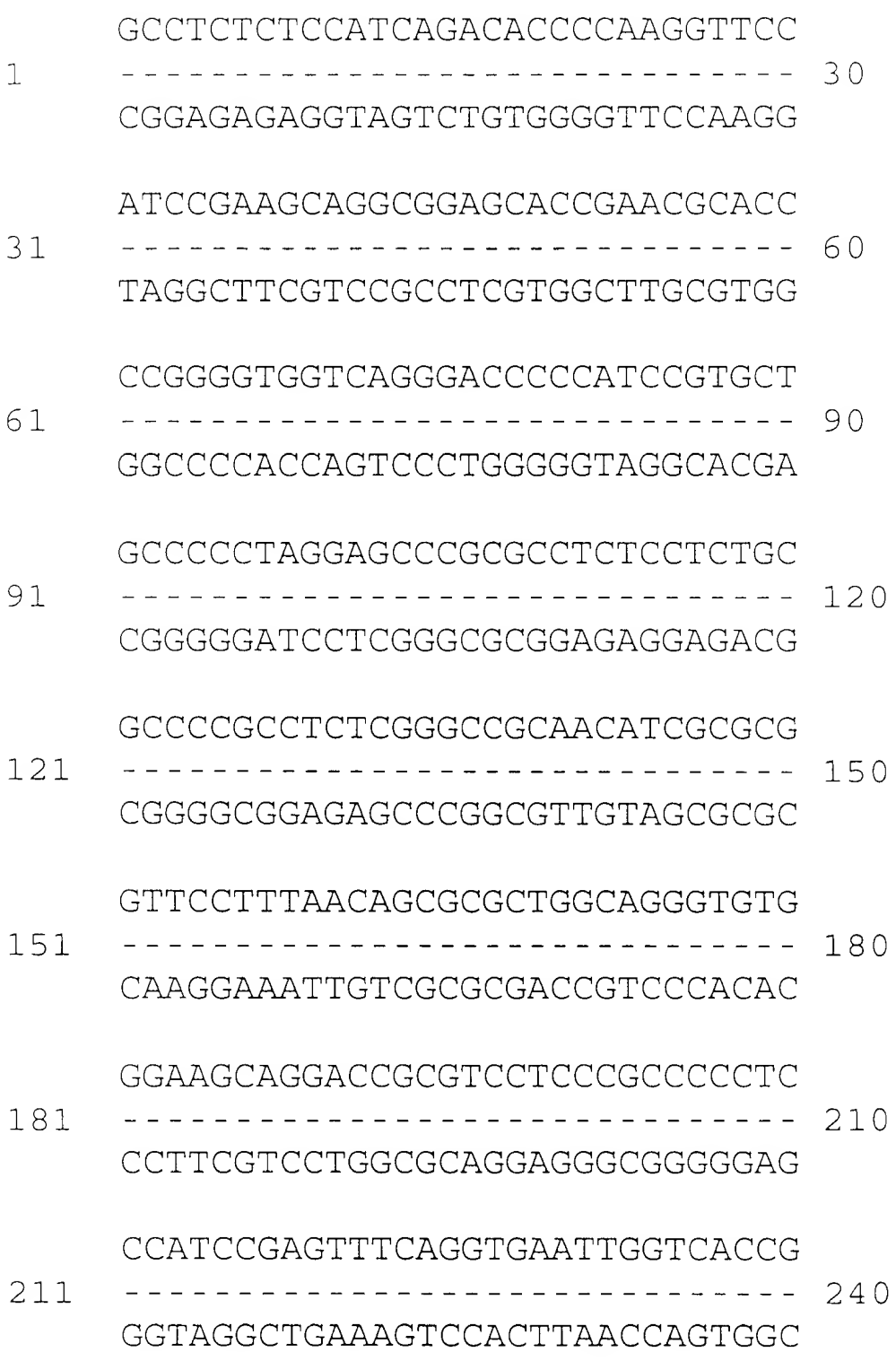
Figure 1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ATCCGAAGCAGGCGGAGCACCGAACGCACC
31 ---------- 60
TAGGCTTCGTCCGCCTCGTGGCTTGCGTGG
CCGGGGTGGTCAGGGACCCCCATCCGTGCT
61 ---------- 90
GGCCCCACCAGTCCCTGGGGGTAGGCACGA
GCCCCCTAGGAGCCCGCGCCTCTCCTCTGC
91 ---------- 120
CGGGGGATCCTCGGGCGCGGAGAGGAGACG
GCCCCGCCTCTCGGGCCGCAACATCGCGCG
121 ---------- 150
CGGGGCGGAGAGCCCGGCGTTGTAGCGCGC
GTTCCTTTAACAGCGCGCTGGCAGGGTGTG
151 ---------- 180
CAAGGAAATTGTCGCGCGACCGTCCCACAC
GGAAGCAGGACCGCGTCCTCCCGCCCCCTC
181 ---------- 210
CCTTCGTCCTGGCGCAGGAGGGCGGGGGAG
CCATCCGAGTTTCAGGTGAATTGGTCACCG
211 ---------- 240
GGTAGGCTGAAAGTCCACTTAACCAGTGGC

```
      AGGGAGGAGGCCGACACACCACACCTACAC
241   ------------------------------ 271
      TCCCTCCTCCGGCTGTGTGGTGTGGATGTG

      TCCCGCGTCCACCTCTCCCTCCCTGCTTCC
271   ------------------------------ 300
      AGGGCGCAGGTGGAGAGGGAGGGACGAAGG

      TCTTGGCGGAGGCGGCAGGAACCGAGAGCC
301   ------------------------------ 330
      AGAACCGCCTCCGCCGTCCTTGGCTCTCGG

      AGGTCCAGAGCGCCGAGGAGCCGGTCTAGG
331   ------------------------------ 360
      TCCAGGTCTCGCGGCTCCTCGGCCAGATCC

      ACGCAGCAGATTGGTTTATCTTGGAAGCTA
361   ------------------------------ 390
      TGCGTCGTCTAACCAAATAGAACCTTCGAT

      AAGGGCATTGCTCATCCTGAAGATCAGCTG
391   ------------------------------ 420
      TTCCCGTAACGAGTAGGACTTCTAGTCGAC
                    START
      ACCATTGACAATCAGCCATGTCATCCAGGC
421   ------------------------------ 450
      TGGTAACTGTTAGTCGGTACAGTAGGTCCG
                        M  S  S  R  P

      CTCTTGAAAGTCCACCTCCTTACAGGCCTG
451   ------------------------------ 480
      GAGAACTTTCAGGTGGAGGAATGTCCGGAC
        L  E  S  P  P  P  Y  R  P  D
```

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```
      ATGAATTCAAACCGAATCATTATGCACCAA
481   ------------------------------ 510
      TACTTAAGTTTGGCTTAGTAATACGTGGTT
        E   F   K   P   N   H   Y   A   P   S

      GCAATGACATATATGGTGGAGAGATGCATG
511   ------------------------------ 540
      CGTTACTGTATATACCACCTCTCTACGTAC
        N   D   I   Y   G   G   E   M   H   V

      TTCGACCAATGCTCTCTCAGCCAGCCTACT
541   ------------------------------ 570
      AAGCTGGTTACGAGAGAGTCGGTCGGATGA
        R   P   M   L   S   Q   P   A   Y   S

      CTTTTTACCCAGAAGATGAAATTCTTCACT
571   ------------------------------ 600
      GAAAAATGGGTGTTCTACTTTAAGAAGTGA
        F   Y   P   E   D   E   I   L   H   F

      TCTACAAATGGACCTCTCCTCCAGGAGTGA
601   ------------------------------ 630
      AGATGTTTACCTGGAGAGGAGGTCCTCACT
        Y   K   W   T   S   P   P   G   V   I

      TTCGGATCCTGTCTATGCTCATTATTGTGA
631   ------------------------------ 660
      AAGCCTAGGACAGATACGAGTAATAACACT
        R   I   L   S   M   L   I   I   V   M

       TGTGCATTGCCATCTTTGCCTGTGTGGCCT
661   ------------------------------ 690
      ACACGTAACGGTAGAAACGGACACACCGGA
        C   I   A   I   F   A   C   V   A   S
```

```
      CCACGCTTGCCTGGGACAGAGGCTATGGAA
691   ------------------------------ 720
      GGTGCGAACGGACCCTGTCTCCGATACCTT
        T   L   A   W   D   R   G   Y   G   T

      CTTCCCTTTTAGGAGGTAGTGTAGGCTACC
721   ------------------------------ 750
      GAAGGGAAAATCCTCCATCACATCCGATGG
        S   L   L   G   G   S   V   G   Y   P

      CTTATGGAGGAAGTGGCTTTGGTAGCTACG
751   ------------------------------ 780
      GAATACCTCCTTCACCGAAACCATCGATGC
        Y   G   G   S   G   F   G   S   Y   G

      GAAGTGGCTATGGCTATGGCTATGGTTATG
781   ------------------------------ 810
      CTTCACCGATACCGATACCGATACCAATAC
        S   G   Y   G   Y   G   Y   G   Y   G

      GCTATGGCTACGGAGGCTATACAGACCCAA
811   ------------------------------ 840
      CGATACCGATGCCTCCGATATGTCTGGGTT
        Y   G   Y   G   G   Y   T   D   P   R

      GAGCAGCAAAGGGCTTCATGTTGGCCATGG
841   ------------------------------ 870
      CTCGTCGTTTCCCGAAGTACAACCGGTACC
        A   A   K   G   F   M   L   A   M   A

      CTGCCTTTTGTTTCATTGCCGCGTTGGTGA
871   ------------------------------ 900
      GACGGAAAACAAAGTAACGGCGCAACCACT
        A   F   C   F   I   A   A   L   V   I
```

Replacement Sheet

```
      TCTTTGTTACCAGTGTTATAAGATCTGAAA
901   ------------------------------ 930
      AGAAACAATGGTCACAATATTCTAGACTTT
        F  V  T  S  V  I  R  S  E  M

      TGTCCAGAACAAGAAGATACTACTTAAGTG
931   ------------------------------ 960
      ACAGGTCTTGTTCTTCTATGATGAATTCAC
        S  R  T  R  R  Y  Y  L  S  V

      TGATAATAGTGAGTGCTATCCTGGGCATCA
961   ------------------------------ 990
      ACTATTATCACTCACGATAGGACCCGTAGT
        I  I  V  S  A  I  L  G  I  M

      TGGTGTTTATTGCCACAATTGTCTATATAA
991   ------------------------------ 1020
      ACCACAAATAACGGTCTTAACAGATATATT
        V  F  I  A  T  I  V  Y  I  M

      TGGGAGTGAACCCAACTGCTCAGTCTTCTG
1021  ------------------------------ 1050
      ACCCTCACTTGGGTTGACGAGTCAGAAGAC
        G  V  N  P  T  A  Q  S  S  G

      GATCTCTATATGGTTCACAAATATATGCCC
1051  ------------------------------ 1080
      CTAGAGATATACCAAGTCTTTATATACGGG
        S  L  Y  G  S  Q  I  Y  A  L

      TCTGCAACCAATTTTATACACCTGCAGCTA
1081  ------------------------------ 1110
      AGACGTTGGTTAAAATATGTGGACGTCGAT
        C  N  Q  F  Y  T  P  A  A  T
```

Sequence Listing

```
     CTGGACTCTACGTGGATCAGTATTTGTATC
1111 ------------------------------ 1140
     GACCTGAGATCGACCTAGTCATAAACATAG
       G  L  Y  V  D  Q  Y  L  Y  H

     ACTACTGTGTTGTGGATCCCCAGGAGGCCA
1141 ------------------------------ 1170
     TGATGACACAACACCTAGGGGTCCTCCGGT
       Y  C  V  V  D  P  Q  E  A  I

     TTGCCATTGTACTGGGGTTCATGATTATTG
1171 ------------------------------ 1200
     AACGGTAACATGACCCCAAGTACTAATAAC
       A  I  V  L  G  F  M  I  I  V

     TGGCTTTTGCTTTAATAATTTTCTTTGCTG
1201 ------------------------------ 1230
     ACCGAAAACGAAATTATTAAAAGAAACGAC
       A  F  A  L  I  I  F  F  A  V

     TGAAAACTCGAAGAAAGATGGACAGGTATG
1231 ------------------------------ 1260
     ACTTTTGAGCTTCTTTCTACCTGTCCATAC
       K  T  R  R  K  M  D  R  Y  D

     ACAAGTCCAATATTTTGTGGGACAAGGAAC
1261 ------------------------------ 1290
     TGTTCAGGTTATAAAACACCCTGTTCCTTG
       K  S  N  I  L  W  D  K  E  H

     ACATTTATGATGAGCAGCCCCCCAATGTCG
1291 ------------------------------ 1320
     TGTAAATACTACTCGTCGGGGGGTTACAGC
       I  Y  D  E  Q  P  P  N  V  E
```

Replacement Sheet - 26 April 2004

```
      AGGAGTGGGTTAAAAATGTGTCTGCAGGCA
1321  ------------------------------ 1350
      TCCTCACCCAATTTTTACACAGACGTCCGT
        E  W  V  K  N  V  S  A  G  T

      CACAGGACGTGCCTTCACCCCCATCTGACT
1351  ------------------------------ 1380
      GTGTCCTGCACGGAAGTGGGGGATGACTGA
        Q  D  V  P  S  P  P  S  D  Y

      ATGTGGAAAGAGTTGACAGTCCCATGGCAT
1381  ------------------------------ 1410
      ATCACCTTTCTCAACTGTCAGGGTACCGTA
        V  E  R  V  D  S  P  M  A  Y

      ACTCTTCCAATGGCAAAGTGAATGACAAGC
1411  ------------------------------ 1440
      TGAGAAGGTTACCGTTTCACTTACTGTTCG
        S  S  N  G  K  V  N  D  K  R

      GGTTTTATCCAGAGTCTTCCTATAAATCCA
1441  ------------------------------ 1470
      CCAAAATAGGTCTCAGAAGGATATTTAGGT
        F  Y  P  E  S  S  Y  K  S  T

      CGCCGGTTCCTGAAGTGGTTCAGGAGCTTC
1471  ------------------------------ 1500
      GCGGCCAAGGACTTCACCAAGTGGTCGAAG
        P  V  P  E  V  V  Q  E  L  P

      CATTAACTTCGCCTGTGGATGACTTCAGGC
1501  ------------------------------ 1530
      GTAATTGAAGCGGACACCTACTCAAGTCCG
        L  T  S  P  V  D  D  F  R  Q
```

```
     AGCCTCGTTACAGCAGCGGTGGTAACTTTG
1531 ------------------------------ 1560
     TCGGAGCAATGTCGTCGCCACCATTGAAAC
       P  R  Y  S  S  G  G  N  F  E

     AGACACCTTCAAAAAGAGCACCTGCAAAGG
1561 ------------------------------ 1590
     TCTGTGGAAGTTTTTCTCGTGGACGTTTCC
       T  P  S  K  R  A  P  A  K  G

     GAAGAGCAGGAAGGTCAAAGAGAACAGAGC
1591 ------------------------------ 1620
     CTTCTCGTCCTTCCAGTTTCTCTTGTCTCG
        R  A  G  R  S  K  R  T  E  Q

     AAGATCACTATGAGACAGACTACACAACTG
1621 ------------------------------ 1650
     TTCTAGTGATACTCTGTCTGATGTGTTGAC
       D  H  Y  E  T  D  Y  T  T  G

     GCGGCGAGTCCTGTGATGAGCTGGAGGAGG
1651 ------------------------------ 1680
     CGCCGCTCAGGACACTACTCGACCTCCTCC
       G  E  S  C  D  E  L  E  E  D

     ACTGGATCAGGGAATATCCACCTATCACTT
1681 ------------------------------ 1710
     TCACCTAGTCCCTTATAGGTGGATAGTGAA
       W  I  R  E  Y  P  P  I  T  S

     CAGATCAACAAAGACAACTGTACAAGAGGA
1711 ------------------------------ 1740
     GTCTAGTTGTTTCTGTTGACATGTTCTCCT
       D  Q  Q  R  Q  L  Y  K  R  N
```

```
     ATTTTGACACTGGCCTACAGGAATACAAGA
1741 ------------------------------ 1770
     TAAAACTGTGACCGGATGTCCTTATGTTCT
       F  D  T  G  L  Q  E  Y  K  S

     GCTTACAATCAGAACTTGATGAGATCAATA
1771 ------------------------------ 1800
     CGAATGTTAGTCTTGAACTACTCTAGTTAT
       L  Q  S  E  L  D  E  I  N  K

     AAGAACTCTCCCGTTTGGATAAAGAATTGG
1801 ------------------------------ 1830
     TTCTTGAGAGGGCAAACCTATTTCTTAACC
       E  L  S  R  L  D  K  E  L  D

     ATGACTATAGAGAAGAAAGTGAAGAGTACA
1831 ------------------------------ 1860
     TACTGATATCTCTTCTTTCACTTCTCATGT
       D  Y  R  E  E  S  E  E  Y  M

     TGGCTGCTGCTGATGAATACAATAGACTGA
1861 ------------------------------ 1890
     ACCGACGACGACTACTTATGTTATCTGACT
       A  A  A  D  E  Y  N  R  L  K

     AGCAAGTGAAGGGATCTGCAGATTACAAAA
1891 ------------------------------ 1920
     TCGTTCACTTCCCTAGACGTCTAATGTTTT
       Q  V  K  G  S  A  D  Y  K  S

     GTAAGAAGAATCATTGCAAGCAGTTAAAGA
1921 ------------------------------ 1950
     CATTCTTCTTAGTAACGTTCGTCAATTTCT
       K  K  N  H  C  K  Q  L  K  S
```

Sequence Listing

```
      GCAAATTGTCACACATCAAGAAGATGGTTG
1951  ------------------------------ 1980
      CGTTTAACAGTGTGTAGTTCTTCTACCAAC
        K   L   S   H   I   K   K   M   V   G
                                    STOP
      GAGACTATGATAGACAGAAAACATAGAAGG
1981  ------------------------------ 2010
      CTCTGATACTATCTGTCTTTTGTATCTTCC
        D   Y   D   R   Q   K   T
      CTGATGCCAAGTTGTTTGAGAAATTAAGTA
2011  ------------------------------ 2040
      GACTACGGTTCAACAAACTCTTTAATTCAT

      TCTGACATCTCTGCAATCTTCTCAGAAGGC
2041  ------------------------------ 2070
      AGACTGTAGAGACGTTAGAAGAGTCTTCCG

      AAATGACTTTGGACCATAACCCCGGAAGCC
2071  ------------------------------ 2100
      TTTACTGAAACCTGGTATTGGGGCCTTCGG

       AAACCTCTGTGAGCATCACAAAGTTTTGGG
2101  ------------------------------ 2130
      TTTGGAGACACTCGTAGTGTTTCAAAACCC

      TTGCTTTAACATCATCAGTATTGAAGCATT
2131  ------------------------------ 2160
      AACGAAATTGTAGTAGTCATAACTTCGTAA

      TTATAAATCGCTTTTGATAATCAACTGGGC
2161  ------------------------------ 2190
      AATATTTAGCGAAAACTATTAGTTGACCCG
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```
     TGAACAACTCCAATTAAGGATTTTATGCTT
2191 ------------------------------ 2220
     ACTTGTTGAGGTTAATTCCTAAAATACGAA

     TAAACATTGGTTCTTGTATTAAGAATGAAA
2221 ------------------------------ 2250
     ATTTGTAACCAAGAACATAATTCTTACTTT

     TACTGTTTGAGGTTTTTAAGCCTTAAAGGA
2251 ------------------------------ 2280
     ATGACAAACTCCAAAAATTCGGAATTTCCT

     AGGTTCTGGTGTGAACTAAACTTTCACACC
2281 ------------------------------ 2310
     TCCAAGACCACACTTGATTTGAAAGTGTGG

     CC
2311 --                             2312
     GG
```

Replacement Sheet - 2005-12-05

Figure 2

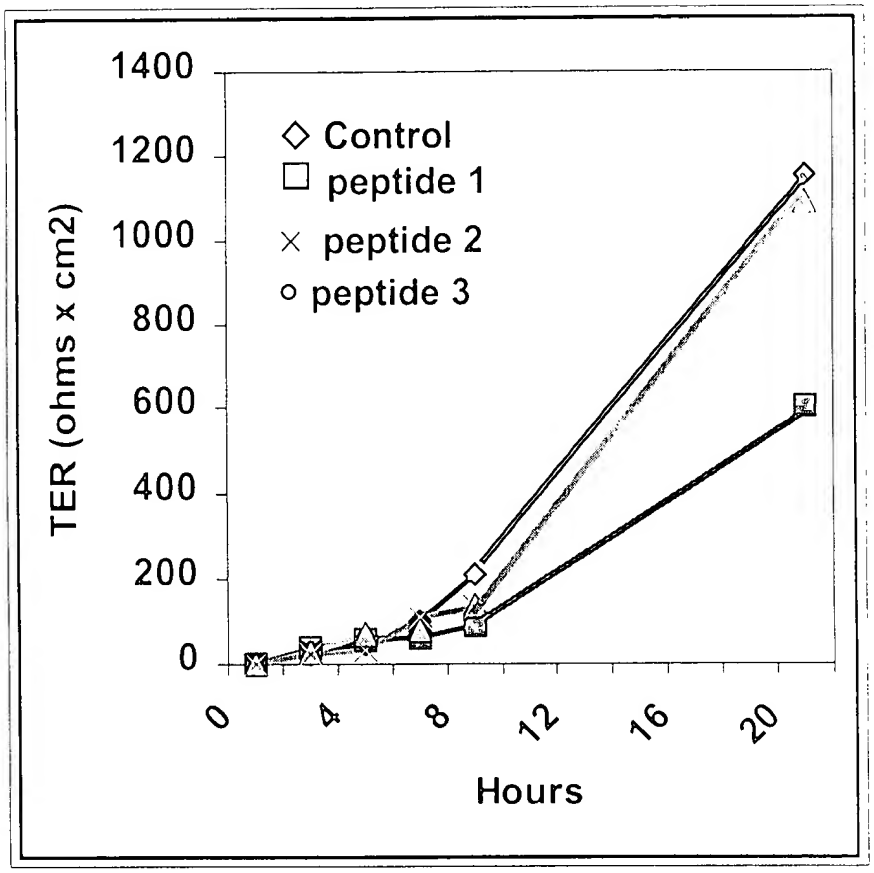

1400
1200
1000
800
600
400
200
0
TER (ohms x cm2)
◇ Control
□ peptide 1
× peptide 2
○ peptide 3
0
4
8
12
16
20
Hours

Figure 3A

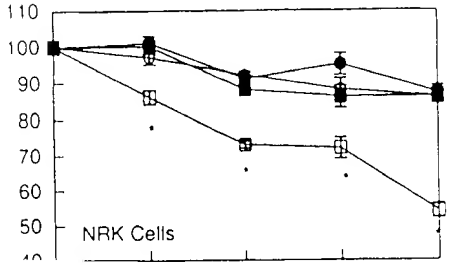


Figure 3B

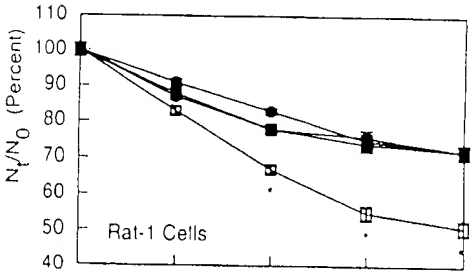
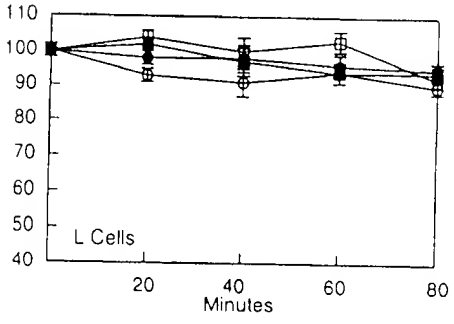


Figure 3C



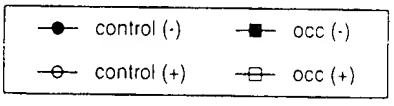


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Figure 4

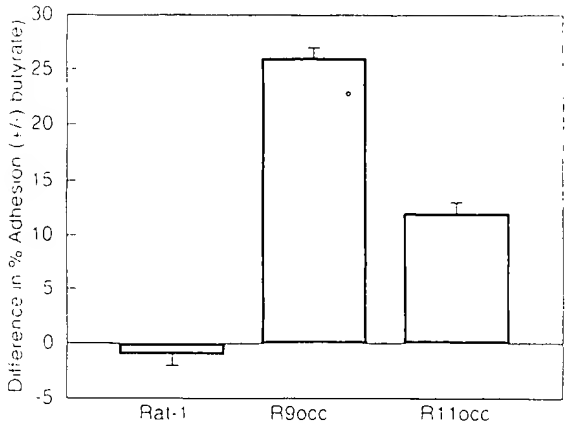

Figure 5A

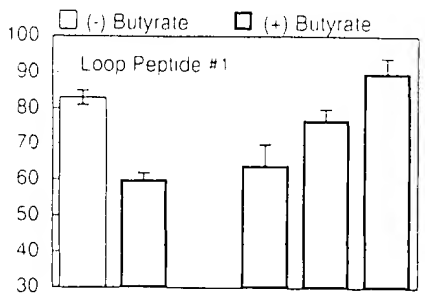

Figure 5B

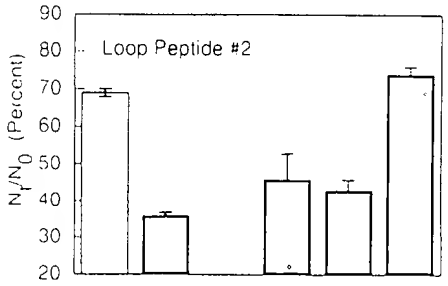
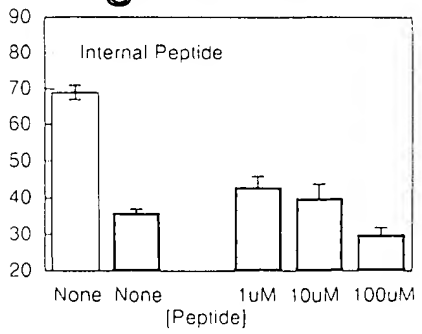
Figure 5C